GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 21:47:54 ; Search time 755.06 Seconds
(without alignments)
27.251 Million cell updates/sec

Title: US-09-851-670-2
Perfect score: 24
Sequence: 1 cgacaaatggaaaaacagctcgcc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15.2	63.3	25	22	AAC92017	PCR primer oJL103.
	2	14.6	60.8	42	14	AAQ38136	Mycobacterium 23S
c	3	14.6	60.8	58	16	AAQ84428	Mycobacterium fort
	4	14.2	59.2	19	21	AAA60233	Human HPC2 cDNA se
	5	14.2	59.2	31	20	AAX06288	Human biallelic po
	6	14.2	59.2	42	21	AAZ99133	B. subtilis HPS/HP
	7	14.2	59.2	45	20	AAX88588	Human chromosome 1
c	8	14.2	59.2	53	22	AAH36592	Human colon cancer
	9	14	58.3	30	21	AAA99037	Human Factor VIII
	10	14	58.3	30	22	AAC67914	Human Factor VIII
	11	14	58.3	30	22	AAC67925	Human TFIXI1 oligo
	12	13.8	57.5	22	22	AAS06892	SNP containing pro
	13	13.8	57.5	32	21	AAF21597	Neisseria ORF 121
	14	13.8	57.5	32	21	AAA81312	N. meningitidis OR
	15	13.8	57.5	32	21	AAZ54567	Neisseria ORF PCR
	16	13.8	57.5	32	21	AAZ54747	Neisseria species
c	17	13.8	57.5	47	21	AAZ66262	Human map-related
c	18	13.6	56.7	31	22	AAI30159	Human single nucle
c	19	13.6	56.7	31	22	AAI31069	Human single nucle
	20	13.4	55.8	30	19	AAV35409	HIV-1 gag protein
	21	13.4	55.8	31	9	AAN80770	Probe for detectio
	22	13.4	55.8	31	10	AAN92231	Probe for HIV-1 vi
	23	13.4	55.8	31	19	AAV67874	Nucleotide fragmen
c	24	13.4	55.8	36	16	AAQ82965	Oligo primer A089/
c	25	13.4	55.8	37	16	AAQ98693	KEX2C 3' PCR prime
	26	13.4	55.8	47	21	AAZ65958	Human map-related
c	27	13.2	55.0	21	19	AAV57381	Primer used to det
c	28	13.2	55.0	29	19	AAV28948	Plasmid pAMG21 hFG
	29	13.2	55.0	31	14	AAQ39026	Mutagenic PCR prim
	30	13.2	55.0	44	21	AAA37491	Arabidopsis thalia
	31	13	54.2	27	18	AAT61708	Prostatic specific
c	32	13	54.2	28	18	AAT94674	Snapdragon flavono
c	33	13	54.2	28	20	AAZ09746	Human HM1.24 antig
c	34	13	54.2	29	22	AAF74794	Human HM1.24 prote
c	35	13	54.2	29	22	AAF74805	Human HM1.24 prote
c	36	13	54.2	35	21	AAZ95727	Clostridium botuli
c	37	13	54.2	41	19	AAV50904	Maize polymorphic
c	38	13	54.2	45	18	AAT96563	Rat neurodap 1 gen
c	39	13	54.2	45	21	AAA95533	TCR alpha-beta cDN
	40	13	54.2	47	21	AAC68529	STE20-like protein
c	41	12.8	53.3	21	19	AAZ26465	Human polymorphic
	42	12.8	53.3	22	22	AAF60111	Human ATM gene exo
	43	12.8	53.3	29	21	AAA04618	Polymorphic fragme
	44	12.8	53.3	32	17	AAT39150	Primer for amplify
	45	12.8	53.3	32	19	AAV45063	FRAP 3' fragment p

ALIGNMENTS

RESULT 1
AAC92017/c
ID AAC92017 standard; DNA; 25 BP.
XX
AC AAC92017;
XX
DT 21-MAR-2001 (first entry)
XX
DE PCR primer oJL103.
XX
KW Heterologous gene expression; transposase; Mos1; mariner-like transposon;
KW PCR primer; ss.
XX
OS Drosophila mauritiana.
XX
PN WO200073510-A1.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US40091.
XX
PR 01-JUN-1999; 99US-0136972.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Bessereau J, Jorgensen E;
XX
DR WPI; 2001-080477/09.
XX
PT Regulating expression of heterologous gene in Caenorhabditis elegans
PT involves inserting transgene construct comprising heterologous gene,
PT especially transposase gene into C.elegans -
XX
PS Example 3; Page 18; 48pp; English.

```
XX
CC   The present invention relates to a method for regulating expression of a
CC   heterologous gene, into Caenorhabditis elegans, which involves inserting
CC   a transgene construct comprising a heterologous gene, preferably a
CC   transposase gene, into C. elegans. The transposon used in the method is
CC   preferably Mos1, a mariner-like transposon isolated from Drosophila
CC   mauritiana. The present sequence is a PCR primer for Mos1, used in the
CC   method of the present invention.
XX
SQ   Sequence 25 BP; 2 A; 3 C; 8 G; 12 T; 0 other;


  Query Match             63.3%;  Score 15.2;  DB 22;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 6.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 caaatggaaaaacagctcgc 23
           |||| | ||||||| |||||
Db      23 CAAACGCAAAAACAACTCGC 4


RESULT   2
AAQ38136
ID   AAQ38136 standard; DNA; 42 BP.
XX
AC   AAQ38136;
XX
DT   01-JUL-1993  (first entry)
XX
DE   Mycobacterium 23S rRNA primer/probe #29.
XX
KW   Primer; probe; 16S; 23S; rRNA; Mycobacteria; subgeneric; class;
KW   rDNA; hybridisation; amplify; PCR; ss.
XX
OS   Synthetic.
XX
PN   WO9304201-A.
XX
PD   04-MAR-1993.
XX
PF   13-AUG-1992;   92WO-US06821.
XX
PR   13-AUG-1991;   91US-0744282.
XX
PA   (STAD ) AMOCO CORP.
XX
PI   Liu J,  Nietupski RM,  Shah JS;
XX
DR   WPI; 1993-094026/11.
XX
PT   Oligo-nucleotide(s) complementary to Mycobacterial ribosomal RNA
PT   or DNA - used for detection and identification of Mycobacterial
PT   in hybridisation and amplification assays
XX
PS   Claim 4; Page 18; 121pp; English.
XX
CC   The sequences given in AAQ38108-46 are primer/probes which correspond
CC   to regions of the 16S and 23S rRNA of Mycobacterial sp. and members
CC   of subgeneric classes.  These oligomers hybridise under assay
CC   conditions to rRNA/rDNA from >90% of common mycobacterium sp., these
CC   oligomers are substantially inclusive.  The primer/probe sequences
CC   given in AAQ38150-59 hybridise to >10% of other bacterial sp.,these are
CC   non-exclusive.  All these oligomers can be used to detect Mycobacterium
CC   and their subgeneric classes by hybridisation or by amplification.
XX
SQ   Sequence 42 BP; 13 A; 14 C; 9 G; 6 T; 0 other;


  Query Match             60.8%;  Score 14.6;  DB 14;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 acaaatggaaaaacagctcgc 23
           | || |||||||||| || |
Db      22 agaactggaaaaacaggtccc 42


RESULT   3
AAQ84428/c
ID   AAQ84428 standard; rRNA; 58 BP.
XX
AC   AAQ84428;
XX
DT   02-OCT-1995  (first entry)
XX
DE   Mycobacterium fortuitum 23S rRNA variable region probe 50.
XX
KW   Mycobacterium; species-specific; detection; ribosomal RNA; 23S rRNA;
KW   variable region; probe; ss.
XX
OS   Mycobacterium fortuitum.
XX
PN   WO9503412-A.
XX
PD   02-FEB-1995.
XX
PF   22-JUL-1994;   94WO-FR00929.
XX
PR   23-JUL-1993;   93FR-0009318.
XX
PA   (INMR ) BIO MERIEUX.
XX
PI   Christen R,  Mabilat C;
XX
DR   WPI; 1995-075238/10.
XX
PT   Single stranded nucleic acid fragments specific for particular
PT   Mycobacterium species  - useful as probes and primers for
PT   detection, identification and amplification, also for therapy,
PT   derived from variable regions of 23S ribosomal RNA
XX
PS   Claim 7; Page 69; 216pp; French.
XX
CC   This sequence is from a variable region of 23S rRNA from
CC   Mycobacterium fortuitum. It is useful as a probe for species-
CC   specific identification of Mycobacteria, pref. in a sandwich assay.
CC   The variable regions were identified by comparison of the 23S rRNA
CC   from many Mycobacterial species; this sequence is from the region
CC   corresp. to nucleotides 289-290 in E.coli 23S rRNA.
XX
SQ   Sequence 58 BP; 10 A; 9 C; 20 G; 19 U; 0 other;


  Query Match             60.8%;  Score 14.6;  DB 16;  Length 58;
  Best Local Similarity   81.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 acaaatggaaaaacagctcgc 23
           | || |||||||||| || |
Db      26 AGAACTGGAAAAACAGGTCCC 6


RESULT   4
AAA60233
ID   AAA60233 standard; DNA; 19 BP.
XX
AC   AAA60233;
XX
DT   07-DEC-2000  (first entry)
XX
DE   Human HPC2 cDNA sequencing primer SEQ ID NO: 54.
XX
KW   Human; mouse; prostate cancer predisposing gene; HPC2;
KW   human chromosome 17p; gene therapy; peptide therapy; drug design;
KW   PCR primer; sequencing primer; ss.
XX
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OS Homo sapiens.
XX
PN WO200027864-A1.
XX
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US26055.
XX
PR 06-NOV-1998; 98US-0107468.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX
DR WPI; 2000-376481/32.
XX
PT Human prostate cancer (HPC)2 nucleic acids, polypeptides, and
PT antibodies, useful for treatment and diagnosis of prostate cancer -
XX
PS Example 3; Page 56; 157pp; English.
XX
CC The present sequence is a primer used in the isolation of the human
CC and murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human
CC version of the gene is found on chromosome 17p. Some alleles cause a
CC predisposition to cancer, particularly prostate cancer. This gene and its
CC protein can be used in peptide and gene therapy for cancer patients, as
CC well as being useful as diagnostic tools (both for cancer sufferers and
CC those with a predisposition to the disease) and in the production of
CC cancer drugs.
XX
SQ Sequence 19 BP; 8 A; 5 C; 3 G; 3 T; 0 other;

Query Match 59.2%; Score 14.2; DB 21; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 caaatggaaaaacagctcg 22
||| |||||||| | ||||
Db 1 caactggaaaaatacctcg 19

RESULT 5
AAX06288
ID AAX06288 standard; DNA; 31 BP.
XX
AC AAX06288;
XX
DT 31-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic DNA fragment SGC30827.
XX
KW Polymorphism; biallelic; paternity testing; forensic; genetic mapping;
KW phenotypic typing; medicament; disease; marker; human; ss.
XX
OS Homo sapiens.
XX
PN WO9858529-A2.
XX
PD 30-DEC-1998.
XX
PF 22-JUN-1998; 98WO-US12930.
XX
PR 24-JUN-1997; 97US-0050594.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Berno A, Chee M, Fan J, Lipshutz RJ;
XX
DR WPI; 1999-080963/07.
XX
PT New nucleic acid segments containing polymorphic sites - used for,
PT e.g. detecting a disease phenotype, in forensics, paternity testing
PT or genetic mapping of phenotypic traits
XX
PS Claim 1; Page 19; 61pp; English.
XX
CC Sequences AAX06101-X06558 represent human DNA fragments which contain
CC biallelic polymorphic markers. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These
CC fragments can be used in a method for determining polymorphic forms in
CC an individual. The invention further provides computer-readable storage
CC medium for storing data for access by an application programme being
CC executed on a data processing system. Such a method comprises a data
CC structure stored in the computer-readable storage medium, the data
CC structure including information resident in a database used by the
CC application programme and including records, each record comprising
CC information identifying a polymorphism shown in the above sequences. The
CC products and methods can be used for analysing polymorphic sites in
CC individuals for testing for the presence of a disease phenotype or in
CC forensics, paternity testing or genetic mapping of phenotypic traits.
CC They can also be used for the production of polypeptides expressed by
CC variant genes and for the production of transgenic animals. The nucleic
CC acid segments can also be used in the manufacture of medicaments for the
CC treatment or prophylaxis of diseases.
XX
SQ Sequence 31 BP; 11 A; 5 C; 7 G; 7 T; 1 other;

Query Match 59.2%; Score 14.2; DB 20; Length 31;
Best Local Similarity 76.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cgacaaatggaaaaacagctc 21
| ||| | ||| |||:|||||
Db 1 ctacatagggataaaasagctc 21

RESULT 6
AAZ99133
ID AAZ99133 standard; DNA; 42 BP.
XX
AC AAZ99133;
XX
DT 21-JUN-2000 (first entry)
XX
DE B. subtilis HPS/HPI genes primer BsYck-G1.
XX
KW Hexulose-phosphate synthase; HPS; hexulose phosphate isomerase; HPI;
KW glucose 6-phosphate; methanol; PCR primer; ss.
XX
OS Bacillus subtilis.
XX
PN JP2000041683-A.
XX
PD 15-FEB-2000.
XX
PF 04-AUG-1998; 98JP-0220881.
XX
PR 04-AUG-1998; 98JP-0220881.
XX
PA (AJIN) AJINOMOTO KK.
XX
DR WPI; 2000-274044/24.
XX
PT Preparation of hexulose-phosphate synthase and hexulose-phosphate
PT isomerase for preparation of 1-13C D-glucose 6-phosphate from
PT C13-labeled methanol -
XX
PS Examples; Page 10; 15pp; Japanese.
XX
CC The invention relates to a novel DNA fragment containing the
CC hexulose-phosphate synthase (HPS) and hexulose phosphate isomerase
CC (HPI) coding sequences (AAZ99132). This sequene represents a PCR primer
CC used to isolate these genes. HPS or HPS and HPI are used for the
CC preparation of C13-D-glucose 6-phosphate from C13-labelled methanol.

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XX
SQ   Sequence 42 BP; 14 A; 7 C; 9 G; 12 T; 0 other;


  Query Match             59.2%;  Score 14.2;  DB 21;  Length 42;
  Best Local Similarity   84.2%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 aaatggaaaaacagctcgc 23
           ||||||||  |||||| ||
Db      12 aaatggaattacagcttgc 30


RESULT   7
AAX88588
ID   AAX88588 standard; DNA; 45 BP.
XX
AC   AAX88588;
XX
DT   10-SEP-1999  (first entry)
XX
DE   Human chromosome 18q YAC clone nucleotide sequence.
XX
KW   Human chromosome 18q; mood disorder; polymorphic marker; detection;
KW   identification; trinucleotide repeat expansion; schizophrenia;
KW   anxiety disorder; adjustment disorder; personality disorder;
KW   nucleotide triplet repeat; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9932643-A2.
XX
PD   01-JUL-1999.
XX
PF   17-DEC-1998;   98WO-EP08543.
XX
PR   18-DEC-1997;   97GB-0026804.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Del-Favero J,  Raeymaekers P,  Van Broeckhoven C;
XX
DR   WPI; 1999-418934/35.
XX
PT   Detecting nucleotide triplet repeats in human chromosome 18q
XX
PS   Disclosure; Page 41; 87pp; English.
XX
CC   The present invention describes detecting nucleotide triplet repeats in
CC   a region of human chromosome 18q disposed between polymorphic markers
CC   D18S68 and D18S979 to identify a human gene associated with a mood
CC   disorder or related disorder. AAX88542 to AAX88705 represents human
CC   chromosome 18q YAC clones and primers corresponding to them, used in the
CC   exemplification of the present invention. YAC clones comprising a
CC   portion of the region of human chromosome 18q between markers D18S68 and
CC   D18S979 are used to identify at least one human gene associated with a
CC   mood disorder or related disorder. The mood disorder or related
CC   disorder, is chosen from the Diagnostic and Statistical Manual of Mental
CC   Disorders, version 4 (DSM-IV) taxonomy. This includes mood disorders
CC   (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related
CC   disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX,
CC   309.81, 308.3), adjustment disorders (309.XX) and personality disorders
CC   (codes 301.XX). Probes derived from genes associated with the mood
CC   disorder or related disorder can be used to detect pathological
CC   mutations or genetic variations in patients. The methods, probes and
CC   antibodies can be used to determine the susceptibility of an individual
CC   to a mood disorder or related disorder. The nucleic acids and proteins
CC   of the human gene can be used to treat mood disorders and related
CC   disorders.
XX
SQ   Sequence 45 BP; 14 A; 7 C; 11 G; 13 T; 0 other;


  Query Match             59.2%;  Score 14.2;  DB 20;  Length 45;
  Best Local Similarity   84.2%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 gacaaatggaaaaacagct 20
           | ||||||  |||| |||||
Db       6 gtcaaatgcaaaatcagct 24


RESULT   8
AAH36592/c
ID   AAH36592 standard; cDNA; 53 BP.
XX
AC   AAH36592;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:3674.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US26524.
XX
PR   29-SEP-1999;   99US-0157137.
PR   03-NOV-1999;   99US-0163280.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG77185.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS   Claim 1; Page 5520-5521; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where
CC   the proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene
CC   therapy and vaccine production. N and P may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate P
CC   expression. For example, N and P may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P by expressing
CC   inactive proteins or to supplement the patients own production of P.
CC   Additionally, N may be used to produce the colon cancer-associated Ps,
CC   by inserting the nucleic acids into a host cell and culturing the cell
CC   to express the proteins. N and P can be used in the prevention, diagnosis
CC   and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC   and AAB77789 represent sequences used in the exemplification of the
CC   present invention.
CC   N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC   missing at time of publication, meaning no sequences are present for
CC   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence 53 BP; 5 A; 11 C; 9 G; 23 T; 5 other;


  Query Match             59.2%;  Score 14.2;  DB 22;  Length 53;
  Best Local Similarity   84.2%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy      6 aatggaaaaacagctcgcc 24
          || || ||||| |||||||
Db     19 AAAGGCAAAACCGCTCGCC 1


RESULT  9
AAA99037
ID   AAA99037 standard; DNA; 30 BP.
XX
AC   AAA99037;
XX
DT   17-JAN-2001  (first entry)
XX
DE   Human Factor VIII PCR fragment oligonucleotide SEQ ID NO:1.
XX
KW   Human; Factor VIII; FVIII; Factor IX truncated intron 1; FIX TI1;
KW   B-domain; modification; gene therapy; PCR; haemostatic;
KW   haemophilia A; ss.
XX
OS   Homo sapiens.
XX
PN   EP1038959-A1.
XX
PD   27-SEP-2000.
XX
PF   17-MAR-1999;   99EP-0104050.
XX
PR   17-MAR-1999;   99EP-0104050.
XX
PA   (AVET ) AVENTIS BEHRING GMBH.
XX
PI   Negrier C,  Plantier JL;
XX
DR   WPI; 2000-603721/58.
XX
PT   Novel modified factor VIII cDNA for use in gene therapy, in which the
PT   wild-type factor VIII cDNA B-domain is deleted and truncated factor IX
PT   intron 1 is inserted in one or more locations -
XX
PS   Disclosure; Page 7; 17pp; English.
XX
CC   The present invention describes a modified Factor VIII (FVIII) cDNA (I)
CC   characterised in that the B-domain of wild-type FVIII cDNA has
CC   been deleted and a truncated Factor IX intron 1 (FIX TI1) has been
CC   inserted in one or more locations of FVIII cDNA. Also described
CC   are: (1) producing FVIII in a cell line containing (I); and
CC   (2) a transfer vector for use in gene therapy comprising (I). (I) has
CC   haemostatic activity, and can be used in gene therapy. (I) is used in
CC   a transfer vector for gene therapy and for a higher yield in vitro
CC   production of FVIII, which is used for treating haemophilia A.
CC   Production of FVIII is improved by adding introns in the FVIII. The
CC   present sequence represents a FVIII PCR fragment oligonucleotide which
CC   is used in the exemplification of the present invention.
XX
SQ   Sequence 30 BP; 9 A; 11 C; 5 G; 5 T; 0 other;


  Query Match           58.3%;  Score 14;  DB 21;  Length 30;
  Best Local Similarity   77.3%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      3 acaaatggaaaaacagctcgcc 24
          ||  ||||||| | ||||| ||
Db      3 acccatggaaatagagctctcc 24


RESULT  10
AAC67914
ID   AAC67914 standard; DNA; 30 BP.
XX
AC   AAC67914;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human Factor VIII oligonucleotide FVIII ATG.
XX
KW   Human; FVIII; Factor VIII; gene therapy; Factor IX intron 1;
KW   Factor VIII production; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1048726-A2.
XX
PD   02-NOV-2000.
XX
PF   03-MAR-2000; 2000EP-0104677.
XX
PR   29-APR-1999;   99EP-0107397.
XX
PA   (CENT-) CENTEON PHARMA GMBH.
XX
PI   Negrier C,  Plantier JL;
XX
DR   WPI; 2001-072945/09.
XX
PT   Modified Factor VIII cDNA comprising a truncated Factor IX intron 1
PT   sequence inserted at one or more locations, useful for efficient
PT   production of Factor VIII in host cells -
XX
PS   Disclosure; Page 9; 19pp; English.
XX
CC   The present sequence is used in an invention relating to a modified
CC   Factor VIII cDNA having a truncated Factor IX intron 1 inserted at one or
CC   more places. The cDNA encodes a mutated Factor VIII, where the wild type
CC   B domain has been deleted. The modified Factor VIII cDNA is used to
CC   generate Factor VIII protein in vitro. The cDNA is used in a transfer
CC   vector for gene therapy. The modification allows increased production of
CC   Factor VIII. Truncated Factor VIII cDNA with an insertion of the Factor
CC   IX intron 1 in intron 1 and 12 and in intron 1 and 13 gave 2-3 and 8-9
CC   times more Factor VIII than unmodified Factor VIII cDNA.
XX
SQ   Sequence 30 BP; 9 A; 11 C; 5 G; 5 T; 0 other;


  Query Match           58.3%;  Score 14;  DB 22;  Length 30;
  Best Local Similarity   77.3%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      3 acaaatggaaaaacagctcgcc 24
          ||  ||||||| | ||||| ||
Db      3 acccatggaaatagagctctcc 24


RESULT  11
AAC67925
ID   AAC67925 standard; DNA; 30 BP.
XX
AC   AAC67925;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human TFIXI1 oligonucleotide FVIII ATG.
XX
KW   Human; FVIII; Factor VIII; gene therapy; truncated Factor IX intron 1;
KW   TFIXI1; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1048726-A2.
XX
PD   02-NOV-2000.
XX
PF   03-MAR-2000; 2000EP-0104677.
XX
PR   29-APR-1999;   99EP-0107397.
XX
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PA (CENT-) CENTEON PHARMA GMBH.
XX
PI Negrier C, Plantier JL;
XX
DR WPI; 2001-072945/09.
XX
PT Modified Factor VIII cDNA comprising a truncated Factor IX intron 1
PT sequence inserted at one or more locations, useful for efficient
PT production of Factor VIII in host cells -
XX
PS Disclosure; Page 12; 19pp; English.
XX
CC The present sequence was used for introducing truncated Factor IX intron
CC 1 into a Factor VIII cDNA sequence. The resulting cDNA encodes a mutated
CC Factor VIII, where the wild type B domain has been deleted. The modified
CC Factor VIII cDNA is used to generate Factor VIII protein in vitro. The
CC cDNA is used in a transfer vector for gene therapy. The modification
CC allows increased production of Factor VIII. Truncated Factor VIII cDNA
CC with an insertion of the Factor IX intron 1 in intron 1 and 12 and in
CC intron 1 and 13 gave 2-3 and 8-9 times more Factor VIII than unmodified
CC Factor VIII cDNA.
XX
SQ Sequence 30 BP; 9 A; 11 C; 5 G; 5 T; 0 other;

Query Match 58.3%; Score 14; DB 22; Length 30;
Best Local Similarity 77.3%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 acaaatggaaaaacagctcgcc 24
|| ||||||| | ||||| ||
Db 3 acccatggaaatagagctctcc 24

RESULT 12
AAS06892
ID AAS06892 standard; DNA; 22 BP.
XX
AC AAS06892;
XX
DT 12-SEP-2001 (first entry)
XX
DE SNP containing protein kinase DNA sequence #61.
XX
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease; SNP;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder; gene therapy; single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
PN WO200138503-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US32085.
XX
PR 24-NOV-1999; 99US-0167482.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
DR WPI; 2001-343950/36.
XX
PT Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections -
XX
PS Example 8B; Page 334; 433pp; English.
XX
CC AAS06832-AAS06897 represent part of a polynucleotide sequence encoding
CC for novel human protein kinases where a single nucleotide polymorphism
CC (SNP) has been identified. The SNP occurs at the last position of the
CC present sequence. The sequences are described relating to the
CC invention of novel human protein kinases #1-57 (AAU03501-AAU03557). The
CC novel protein kinases have been identified as members of the tyrosine
CC or serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be
CC used for gene therapy and as DNA probes in diagnostic assays.
CC The protein kinase polypeptides may be used as antigens in the production
CC of antibodies against the protein kinases and in assays to identify
CC modulators of protein kinase expression and activity.
XX
SQ Sequence 22 BP; 6 A; 6 C; 4 G; 5 T; 1 other;

Query Match 57.5%; Score 13.8; DB 22; Length 22;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 tggaaaaacagctcgcc 24
|| |||||||||| |||
Db 5 tgcaaaaacagctggcc 21

RESULT 13
AAF21597
ID AAF21597 standard; DNA; 32 BP.
XX
AC AAF21597;
XX
DT 13-MAR-2001 (first entry)
XX
DE Neisseria ORF 121 PCR primer SEQ ID NO:98.
XX
KW Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
KW PCR primer; ss.
XX
OS Neisseria sp.
XX
PN WO200066791-A1.
XX
PD 09-NOV-2000.
XX
PF 08-MAR-2000; 2000WO-US05928.
XX
PR 30-APR-1999; 99US-0132068.
PR 08-OCT-1999; 99WO-US23573.
PR 28-FEB-2000; 2000GB-0004695.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Masignani V;
PI Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;
PI Frazer CM, Grandi G;
XX
DR WPI; 2000-647603/62.
XX
PT Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect, treat and prevent Neisserial infections -
XX
PS Example 1; Page 116; 692pp; English.
XX

CC The present invention describes the full length genome of
CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
CC to AAF21613 represent fragments of the NMB genomic sequence, as the
CC sequence was too long to go in a record on its own it was split into 8
CC sequences which overlap each other at the beginning and end of each
CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
CC the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at
CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
CC Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
CC AAF21606 represent PCR primers which are used in the exemplification of
CC the present invention. The NMB genome and fragments from it have
CC antibacterial activity, and can be used in vaccines and gene therapy.
CC Neisseria nucleic acids, proteins and/or antibodies which binds to the
CC proteins can be used in compositions for treating or preventing infection
CC due to Neisserial bacteria or as a diagnostic reagent for detecting the
CC presence of Neisserial bacteria or of antibodies raised to Neisserial
CC bacteria. Computers, computer memory, computer storage medium or computer
CC databases can be used in a search to identify open reading frames (ORFs)
CC or coding sequences within the NMB genome. The DNA sequences provide
CC further opportunities to find antigenic or immunogenic proteins which are
CC more effective in vaccines than the outer membrane proteins currently
CC used.
XX
SQ Sequence 32 BP; 10 A; 9 C; 6 G; 7 T; 0 other;

Query Match 57.5%; Score 13.8; DB 21; Length 32;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 caaatggaaaaacagct 20
|| ||||||| ||||||
Db 10 catatggaaacacagct 26

RESULT 14
AAA81312
ID AAA81312 standard; DNA; 32 BP.
XX
AC AAA81312;
XX
DT 04-DEC-2000 (first entry)
XX
DE N. meningitidis ORF121 PCR primer SEQ ID NO:1058.
XX
KW Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; PCR primer; ss.
XX
OS Neisseria meningitidis.
XX
PN WO200022430-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US23573.
XX
PR 09-OCT-1998; 98US-0103794.
PR 30-APR-1999; 99US-0132068.
XX
PA (CHIR) CHIRON CORP.
XX
PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX
DR WPI; 2000-318079/27.
XX
PT Isolated nucleotide sequences of Neisseria meningitidis which can be
PT used in the diagnosis and treatment of N. meningitidis infection and
PT other Neisserial infections, for example, N.gonorrhoea -
XX
PS Example 1; Page 115; 1760pp; English.
XX
CC The present invention describes methods of obtaining immunogenic
CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC against them, can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC Neisserial bacteria. For example, some of the identified proteins could
CC be components of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neissariae. Identification of sequences
CC from the bacterium will also facilitate production of biological probes,
CC particularly organism-specific probes. Attempts to make efficacious
CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
CC sequences may provide an opportunity to identify secreted or surface
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
CC other more variable regions.
XX
SQ Sequence 32 BP; 10 A; 9 C; 6 G; 7 T; 0 other;

Query Match 57.5%; Score 13.8; DB 21; Length 32;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 caaatggaaaaacagct 20
|| ||||||| ||||||
Db 10 catatggaaacacagct 26

RESULT 15
AAZ54567
ID AAZ54567 standard; DNA; 32 BP.
XX
AC AAZ54567;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria ORF PCR primer SEQ ID NO:3029.
XX
KW Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy; PCR primer; ss.
XX
OS Synthetic.
OS Neisseria sp.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.

XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI; 2000-062150/05.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics
XX
PS Example 1; Page 70; 1453pp; English.
XX
CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrheae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 32 BP; 10 A; 9 C; 6 G; 7 T; 0 other;

Query Match 57.5%; Score 13.8; DB 21; Length 32;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4 caaatggaaaaacagct 20
           || ||||||| ||||||
Db      10 catatggaaacacagct 26
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